

SEQUENCE LISTING

<110> Albani, Salvatore

<120> METHODS FOR ISOLATION, QUANTIFICATION,
CHARACTERIZATION AND MODULATION OF
ANTIGEN-SPECIFIC T CELLS

<130> 031544.0004.CIP

<140> NOT YET ASSIGNED

<141> 2001-01-09

<150> 60/105,018

<151> 1998-10-20

<150> 09/421,506

<151> 1999-10-19

<150> PCT/US99/2466

<151> 1999-10-19

<160> 24

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide derived from third hyper V
region of IE molecule Mus musculus

<400> 1

Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys
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Ala

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide derived from bole I protein
of Epstein Barr virus

<400> 2

Thr Arg Asp Asp Ala Glu Tyr Leu Leu Gly Arg Glu Ser Val Leu
1 5 10 15

<210> 3
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide derived from the hemophilus influenza virus

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Thr Ser Phe Pro Met Arg Gly Asp Leu Ala Lys Arg Glu Pro Asp Lys
1 5 10 15

<210> 4
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide derived from the TCR receptor gene of Mus musculus

<400> 4
Leu His Ile Ser Ala Val Asp Pro Glu Asp Ser Ala Val Tyr Phe Cys Ala Ser
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Ser Gln Glu Phe Phe Ser Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr
20 25 30
Arg Leu
35

<210> 5
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide derived from the influenza virus

<400> 5
Gly Ile Leu Gly Phe Val Phe Thr Leu
1 5

<210> 6
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide derived from the influenza virus

<400> 6
Val Lys Leu Gly Glu Phe Tyr Asn Gln
1 5

<210> 7
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide totally artificial

<220>
<223> Xaa in position 2 stands for cyclohexylalanine

<400> 7
Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala
1 5 10

<210> 8
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide derived from the influenza virus

<400> 8
Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

<210> 9
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide derived from the ovalbumin
of *Mus musculus*

<400> 9
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1 5 10 15
Arg

<210> 10
<211> 15
<212> PRT
<213> *E. coli*

<220>
<223> dnaJpl heat shock protein

<400> 10
Gln Lys Arg Ala Ala Tyr Asp Gln Tyr Gly His Ala Ala Phe Glu
1 5 10 15

<210> 11
<211> 15
<212> PRT
<213> Homo sapiens

<400> 11
Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly
1 5 10 15

<210> 12
<211> 9
<212> PRT
<213> Homo sapiens

<400> 12
Gly Ile Leu Gly Phe Val Phe Thr Leu
1 5

<210> 13
<211> 9
<212> PRT
<213> Homo sapiens

<400> 13
Val Lys Leu Gly Glu Phe Tyr Asn Gln
1 5

<210> 14
<211> 13
<212> PRT
<213> Homo sapiens

<400> 14
Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

<210> 15
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion constructs with human and bacterial sequences

<400> 15
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
1 5 10 15
Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
20 25 30
Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu

35	40	45
Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile		
50	55	60
Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp		
65	70	75
Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr		
85	90	95
Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly		
100	105	110
Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg		
115	120	125
Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr		
130	135	140
Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile		
145	150	155
Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu		
165	170	175
Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp		
180	185	190
Pro Glu Thr Glu Leu Tyr Ala Val Ser Glu Phe Gly Gly Ser Gly Gly		
195	200	205
Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn		
210	215	220
Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser		
225	230	235
Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala		
245	250	255
Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys		
260	265	270
Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr		
275	280	285
Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His		
290	295	300
Ala Ile Ala Ala Ile Ser Met Ala Asn		
305	310	

<210> 16
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion constructs with human and bacterial sequences

<400> 16

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gaagtgaaAG aagtggcaAC gctgtcctgt ggtcacAAAtg tttctgttGA agagctggca 180
caaactcgca tctactggca aaaggagaAG aaaatggtgc tgactatgat gtctggggac 240
atgaatatat ggcccgagta caagaaccgg accatcttG atatcaactaa taacctctcc 300
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gacttcccta caccttagtAt ctctgacttt gaaattccaa cttctaataat tagaaggata 480
atttgctcaa cctctggagg tttccagAG cctcacctct cctgggttGGA aaatggagaa 540
gaattaaatG ccatcaacac aacagttcC caagatcctG aaactgagct ctatgctgtt 600
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 ctagctggaa aaagagagat ggctatcatt actttaaga atggtgcac tttcaagta 780
 gaagtaccag gtatcaaca tatagattca caaaaaaaaaag cgattgaaag gatgaaggat 840
 accctgagga ttgcatatct tactgaagct aaagtcgaaa agttatgtt atgaaataat 900
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<210> 17
 <211> 1056
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fusion constructs with human and bacterial sequences

<400> 17
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 aaccaaagcc ttagtgagct agtagtattt tggcaggacc aggaaaaactt ggttctgaat 180
 gaggtatact taggcaaaga gaaatttgac agtgcattt ccaagtatat gggccgcaca 240
 agtttgatt cggacagttg gaccctgaga ctccacaatc ttcagatcaa ggacaagggc 300
 ttgtatcaat gtatcatcca tcacaaaaag cccacaggaa tgattcgcat ccaccagatg 360
 aattctgaac tgtcagtgtct tgcttaacttc agtcaacactg aaatagtacc aatttcta 420
 ataacagaaa atgtgtacat aaatttgacc tgctcatcta tacacggtta cccagaacct 480
 aagaagatga gtgtttgct aagaaccaag aattcaacta tcgagttatga tggtattatg 540
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 cttttatctt cactttctc tatagagctt gaggaccctc agcctcccc agaccacgaa 720
 ttccggcggct ccgggtggtag cgccacaccc caaaatatta ctgatttgc tgcagaatac 780
 cacaacacac aaatacatac gctaaatgat aagatattt cgtatacaga atctctagct 840
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<210> 18
 <211> 351
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion constructs with human and bacterial sequences

<400> 18
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 1 5 10 15
 Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
 20 25 30
 Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
 35 40 45
 Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
 50 55 60
 Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
 65 70 75 80
 Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
 85 90 95

Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr
 100 105 110
 Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala
 115 120 125
 Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn
 130 135 140
 Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro
 145 150 155 160
 Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr
 165 170 175
 Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp
 180 185 190
 Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met
 195 200 205
 Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser
 210 215 220
 Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu
 225 230 235 240
 Phe Gly Gly Ser Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu
 245 250 255
 Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile
 260 265 270
 Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile
 275 280 285
 Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln
 290 295 300
 His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu
 305 310 315 320
 Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp
 325 330 335
 Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
 340 345 350

<210> 19

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptides

<400> 19

Ser Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala
 1 5 10 15
 Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln
 20 25 30

<210> 20
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> peptides

<400> 20
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1 5 10 15
Leu Lys Gln Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln
20 25 30

<210> 21
<211> 1095
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion constructs with human and bacterial sequences

<400> 21
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cctgaccaat caggcgagtt tatgtttgac tttgatggtg atgagatttt ccatgtggat 180
atggcaaaga aggagacggt ctggcggctt gaagaatttg gacgattgc cagctttag 240
gctcaaggtg cattggccaa catagctgtg gacaaagcca acctggaaat catgacaaag 300
cgctccaact atactccgat caccaatgtt cctccagagg taactgtgct cacgaacagc 360
cctgtggAAC tgagagagcc caacgtcctc atctgttca tcgacaaggta caccggacca 420
gtggtaatg tcacgtggct tcgaaaatgga aaacctgtca ccacaggagt gtcagagaca 480
gtcttcctgc ccagggaaaga ccacctttc cgcaagttcc actatctccc cttctgccc 540
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aagcaactggg agttttagtc tccaagccct ctcccaagaga ctacagagga attcggttgt 660
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ctggaatggg aactgcaggc gctggaaaaaa gaactggcgc agggcggctc cggtggtagc 780
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attacttta agaatgggtgc aactttcaa gttagaagtac caggttagtca acatatacg 960
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<210> 22
<211> 364
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion constructs with human and bacterial sequences

<400> 22
Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
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20 25 30

Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
 35 40 45
 Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
 50 55 60
 Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
 65 70 75 80
 Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
 85 90 95
 Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
 100 105 110
 Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
 115 120 125
 Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
 130 135 140
 Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
 145 150 155 160
 Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
 165 170 175
 Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
 180 185 190
 Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
 195 200 205
 Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser
 210 215 220
 Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln
 225 230 235 240
 Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly
 245 250 255
 Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu
 260 265 270
 Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr
 275 280 285
 Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys
 290 295 300
 Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
 305 310 315 320
 Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala
 325 330 335
 Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys
 340 345 350
 Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
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<210> 23
 <211> 861
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fusion constructs with human and bacterial sequences

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 aaacatgagt gtcattttttt caacgggacg gagcgggtgc ggttccttggaa cagatacttc 180
 tatcaccaag aggagtaacgt ggcgttcgac agcgacgtgg gggagtaccg ggcggtgacg 240

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 cagcgccgag tctatcctga ggtgactgtg tatcctgcaa agaccagcc cctgcagcac 420
 cacaacctcc tggctgctc tgtgaatggt ttctatccag gcagcattga agtcaggtgg 480
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 acctgccaag tggagcaccc aagcctgacg agccctctca cagtggaaatg gagagcacgg 660
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<210> 24

<211> 285

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

<400> 24

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			20						25						30
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					35			40							45
Gly	Thr	Glu	Arg	Val	Arg	Phe	Leu	Asp	Arg	Tyr	Phe	Tyr	His	Gln	Glu
					50			55			60				
Glu	Tyr	Val	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Thr
					65			70			75				80
Glu	Leu	Gly	Arg	Pro	Asp	Ala	Glu	Tyr	Trp	Asn	Ser	Gln	Lys	Asp	Leu
					85				90						95
Leu	Glu	Gln	Lys	Arg	Ala	Ala	Val	Asp	Thr	Tyr	Cys	Arg	His	Asn	Tyr
					100				105						110
Gly	Val	Gly	Glu	Ser	Phe	Thr	Val	Gln	Arg	Arg	Val	Tyr	Pro	Glu	Val
					115			120			125				
Thr	Val	Tyr	Pro	Ala	Lys	Thr	Gln	Pro	Leu	Gln	His	His	Asn	Leu	Leu
					130			135			140				
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					145			150			155				160
Phe	Arg	Asn	Gly	Gln	Glu	Glu	Lys	Thr	Gly	Val	Val	Ser	Thr	Gly	Leu
					165				170						175
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					180			185			190				
Val	Pro	Arg	Ser	Gly	Glu	Val	Tyr	Thr	Cys	Gln	Val	Glu	His	Pro	Ser
					195			200			205				
Leu	Thr	Ser	Pro	Leu	Thr	Val	Glu	Trp	Arg	Ala	Arg	Ser	Glu	Ser	Ala
					210			215			220				
Gln	Ser	Lys	Gly	Gly	Ser	Gly	Gly	Ser	Ala	Gln	Leu	Lys	Lys	Lys	Leu
					225			230			235				240
Gln	Ala	Leu	Lys	Lys	Asn	Ala	Gln	Leu	Lys	Gln	Lys	Leu	Gln	Ala	
					245			250			255				
Leu	Lys	Lys	Lys	Leu	Ala	Gln	Gly	Ser	Gly	Gly	Ser	Ala	Gly	Gly	
					260			265			270				
Leu	Asn	Asp	Ile	Phe	Glu	Ala	Gln	Lys	Ile	Glu	Trp	His			
					275			280			285				